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Exhibit A

Pairwise Alignment

Sequence 1: Fig.11A 5393670

Sequence 2: SEQIDNO1 09/888,224

Optimal Global alignment

Alignment score: -1036

Identities: 0.34

Fig.11A 5393670	1	-----	1
SEQIDNO1 09/888,224	1	atgataaacgttgcaacgggagaggagaccccaatacacctctttggaagtcaactgggttc	60
Fig.11A 5393670	1	-----	1
SEQIDNO1 09/888,224	61	ggctttgagacaccgaactacgttgttcacggcctatggagtaggaactgggaggacatg	120
Fig.11A 5393670	1	-----	1
SEQIDNO1 09/888,224	121	ctcctccagatcaagagccttggttcaatgcgataagggttccttctgtacctcagtca	180
Fig.11A 5393670	1	-----	1
SEQIDNO1 09/888,224	181	gtaaaaccggggacgatgccaacggcgattgactacgccaaagaaccagacctccagggt	240
Fig.11A 5393670	1	-----	1
SEQIDNO1 09/888,224	241	cttgacagcgtccagataatggagaaaaataatcaagaaggctgggagacctgggcatttc	300
Fig.11A 5393670	1	-----TTG---T---CCG---A-AA-ATGG---C---G---CGTC-A-GTT-A-C-AC	29
SEQIDNO1 09/888,224	301	gtgctccrccacacacagagaattgggttcaacttatagaacecccatgggtacacggac	360
Fig.11A 5393670	30	TGCC-GTT-GA-CAG-CCG--CAI-----CTGC-CC--A-TTC-CCC--GGCTCGGTGC-	72
SEQIDNO1 09/888,224	361	aacttctcggagggagatacataaaacagattgggttgaugtccccagagattccgggaag	420
Fig.11A 5393670	72	--C---CCCC---A-----CCA-A-CC---G---GT---G-CA---C---CCCCCG---A	102
SEQIDNO1 09/888,224	421	tactggaaagtttccggcggggacttaaaagccaaccccacactcaaggccccacact	480
Fig.11A 5393670	103	G---C-----T---CC---A-TC---CGAAATTAC-AA--CTTAG--GT-----G---AAC	135
SEQIDNO1 09/888,224	481	ccccctacacggagggaagtggggccatgggggaattgggaatttcgccaccacactgg	540
Fig.11A 5393670	136	A-----ATTCC--GGCGTGCG--TTC-----CCCACA--CAACTVGGI-GGTCC--	176
SEQIDNO1 09/888,224	541	aacctggcgggttaaaagcaagaaaggaattctgggaattgcccacaatatgggtata	600
Fig.11A 5393670	176	----TTGACTTG-----A-----ACTT--CGGTGCG--GCAGTAC--G--G-AA----ACTAC	214
SEQIDNO1 09/888,224	601	tttgtttgggaaccccggttcaccccccagagatagacgtagtataagtggggccac	660
Fig.11A 5393670	215	A-----CTCTTCACCTC-AA-----GCCCG-----CG-TCAA-----C---	244
SEQIDNO1 09/888,224	661	aacgcctgggtggggagaaaccttatgggtgttagaaattaccaatttaacctgccagg	720
Fig.11A 5393670	244	-ACC-C---CC--TCN-----C-----C-----TGAAGAG-----C	267
SEQIDNO1 09/888,224	721	gnaagggttttttataccccaaagttaaagggttagaagtttacccacacccctacttt	780
Fig.11A 5393670	268	G---CG-----TG-EG---T-CG-----GA-C-TCCCTATCG-----CGG--C	298
SEQIDNO1 09/888,224	781	gacccgggtgagggttccccagaaacctccccgaattatgggaacacacttccactac	840
Fig.11A 5393670	299	GTCG-AA-T-A---C-F-----CC-----GCC-T-CF-CKRGTC-ACCAC-T	329
SEQIDNO1 09/888,224	841	ataaagattggtctgtgttaccctgtgtgttataggtaagtcggaaggaagtaacggcat	900
Fig.11A 5393670	330	CCTTC-A-----CACCC---TCACCA---TGGACCA-----TTC-----ATGCCCGG	367
SEQIDNO1 09/888,224	901	gggtgggaacccggggatglaattggcalkkkaataaatagnrtggatgalccagaa	960
Fig.11A 5393670	368	AG---CTCTGGGG---CTAG---ACCAACGTCT---CTCF---T-----CTCTTA-T	406
SEQIDNO1 09/888,224	961	aaatttggaattcttcttatgtggatgtgaaccaaagagggtgacacctggaatt	1020
Fig.11A 5393670	407	CTCCT-T---DADCT--T-----A-CG-T---AGTAAGTGCTGCT---T---CGCTA--	446
SEQIDNO1 09/888,224	1021	etgaagatatacgggacacaaattgtggagacaaatcaaacacctaaagggttctgtg	1080
Fig.11A 5393670	446	-ACGG-----CAAGAGCTA-GCTTGAGCH-CAAGTCTTGTG-TCT-----T-	487
SEQIDNO1 09/888,224	1081	gaagattgtttttaaacaccacaggccctccctcccaagaaacacacaacaac	1140
Fig.11A 5393670	487	---CCCT-----GIG---GA---GA---GA---AGGCG-----CGCT	510
SEQIDNO1 09/888,224	1141	acacccaacgaccacaacgacacaacatccctccacgacacacaccagaccag	1200
Fig.11A 5393670	510	-TATG-TGTUTAG--TGAGG--GA--ACGGGGG--G-----CC---AA---CCA	549
SEQIDNO1 09/888,224	1201	acacacactatacactacaaaccccccaccaaactccttaataacgtccca	1260

Fig.11A 5393670 549 ---G---TA-TAA---GAGGCGTGGCA-CTAA---GCG---A---GCGGCT 584
SEQIDNO1 09/888,224 1261 tttaaaatgtgacgttctctcgaactauctctcngttagaggaaccgctgaggtt 1320

Fig.11A 5393670 585 AC-TGCCAT-CT-CTCACTCCCGCTCCAG-ACAT---GAA---G---AC---GCGCC 628
SEQIDNO1 09/888,224 1321 gtatgtatgaaaccagctctga-tccagcgttggggaactccgaacctctggaggt 1379

Fig.11A 5393670 629 C-----TC-----AA--G-AF-TAGCAACCGGGCTCT-CTCTCAACAGAGTGA-TA 671
SEQIDNO1 09/888,224 1380 gtttaaaatgggaa-cgpcacgaaggaacccacacttggggtctgggggacgtttca 1439

Fig.11A 5393670 672 TCCTGG-----AGGGCAACTCGA---G---GCG---AATTC---CTT--G-ACC-----G- 707
SEQIDNO1 09/888,224 1440 gattccacccccgaacttggaicccacacacaaaagttagaga-aaggaaaggggtgt 1499

Fig.11A 5393670 708 C-----TC-----GCTCTTCAAGGCCAG-GGGCTG---G-----ACTCT-CT-----C 741
SEQIDNO1 09/888,224 1500 caaggttataaactctctgaatatacatgacccgaatataacaaaggtacaccc 1559

Fig.11A 5393670 742 C--GG-----TTCGCTTTCAACCCCTATCC-----CA-GA-----GGCTAC-AAA-----A 779
SEQIDNO1 09/888,224 1560 ggaggtcatalacggggttaggttgggtcaacagcgaataaacgctcgaacttcgt 1619

Fig.11A 5393670 780 GCT-AT--T--ACT-----GCCCCG--GATAG-KUTT-----G-ACAG-CTC-- 813
SEQIDNO1 09/888,224 1620 gttccgataaagttctcccaacttcgaggaactcttagacacaaagtacacgttga 1679

Fig.11A 5393670 814 CAAGACCTT-----GCAATATC-----ACT---GAGTTC-----CACGGA 849
SEQIDNO1 09/888,224 1680 aagaggttcccggaagaaatagcttttgaggttgggtctgaagggtgcacaa 1739

Fig.11A 5393670 850 CAAC--GGG-TG---GCCCTCGG-----CA-AC-CTT--GAGCATACCGGAATACCA 897
SEQIDNO1 09/888,224 1740 cttgaggtacaggttaggtactacgggttaaggaacagctctacatgggggg 1799

Fig.11A 5393670 898 GCA--AA--GGGTGAG--A-TCCCCACGCGCGGCGCGG---GAC-C-----CC- 943
SEQIDNO1 09/888,224 1800 ctatcctgggttaggaagggggcatttttccggttatattccatattcgtga 1859

Fig.11A 5393670 943 ---A-----TCI-----G-TT-----GCGCCCTTCCGCT---G--A-KCTAC-GCC 977
SEQIDNO1 09/888,224 1860 tggagggttgaacaaatattttgaggtctaaagttataggggttgggtatga 1919

Fig.11A 5393670 978 C-----G---TCCTGCTC-----GTGGG---G---C-----TGA--G----- 1005
SEQIDNO1 09/888,224 1920 tttcttcaccttaaaatataaggaactaacggttagaggttgttttactacac 1979

Fig.11A 5393670 1005 ---GCG-GC---ATG---G-GCTTTGT-T---GAGATTGGAAGGAGAG 1047
SEQIDNO1 09/888,224 1980 caaatctataaaatagttacaacacgttggcggttgcacacacacttact 2039

Fig.11A 5393670 1048 CCAGTAAAT-CT-----GTTT-----GTGGCACT-CTAGG-----CCGAC-G 1085
SEQIDNO1 09/888,224 2040 gatgtcctgaattcgggttcgaatataacacacgttgcctcattccatga 2099

Fig.11A 5393670 1086 C-----G-----TCGAGC-ACC---GATGCA-----GCTTCCAC----- 1118
SEQIDNO1 09/888,224 2100 agtggagtaagggtggtcttgtaagtacattctcctggcggggaactggc 2159

Fig.11A 5393670 1119 TCG-----GAG---AA-----G-----G---CAAG 1138
SEQIDNO1 09/888,224 2160 cactgaggatgaggttctcgtggaggggtccggcctccgcttcataaag 2219

Fig.11A 5393670 1139 A-TG---ACTTGT-T-----GTCACATGGAAGGGGAGATTGGGT-AG 1185
SEQIDNO1 09/888,224 2220 attagagaaataatcaaccacaacacacgcaataccactatcacactag 2279

Fig.11A 5393670 1186 TAGGAATTGGAGG-GCCCTCGCTCTGTGTGGAGAG-ATTTCAG----- 1239
SEQIDNO1 09/888,224 2280 tttaaccacaaataaagaaactacaggtgaaatccaggaacttcagaggtaat 2339

Fig.11A 5393670 1240 T-CAGGGAG--GCTCCTCTCTCGACACCTCTCTGACGCAAT-TCACTTGGG 1297
SEQIDNO1 09/888,224 2340 taaggtcatttcgaggaactggggaactggggaagcccaatttaagggaagaa 2399

Fig.11A 5393670 1298 CACTG-----CT---GG-CAATGGG-TAC-GAG---GTG---G---G---G---GT 1340
SEQIDNO1 09/888,224 2400 ggaaccacaaatctctatataaaatgaacacttaaatctatggggttaaggt 2459

Fig.11A 5393670 1341 GGGC-C-T-AGGTCGCTATAGG-AA-TACTAT---ACT-TC-TA-TGCT---TAG 1390

SEQIDNO1 09/888,224 2460 caccgagaggaacaaacatgagagggggtctccactacgtccagccctggatag 2519

Fig.11A 5393670 1391 AGCGTGACT 1400

SEQIDNO1 09/888,224 2520 tataatgatga 2529

Fig.11A 5393670 1 ----- 1
SEQIDNO1 09/888,224 1 MINVATGEETPIHLFGVNWFGFETPNYVVHGLWSRNWEDMLLQIKSLGFNAIRLPFCTQS 60

Fig.11A 5393670 1 -----XXXP-XXW-X-XXXXXX 15
SEQIDNO1 09/888,224 61 VKPGTMPTAIDYAKNPDLQGLDSVQIMEKIIKKAGDLGIFVLLDYHRIGCNFIEPWWYTD 120

Fig.11A 5393670 16 CXXDHGXX-XXXXXXXXLVXXXP-X-XXPX-V-XXXTXXXX-XXXXXXXXKLXXXYKX-XY 68
SEQIDNO1 09/888,224 121 SFSEQDYINTVEVAQRFGKYWNVIGDLKNEPHSSSAPAAAYTDGSGATWGMGNATDW 180

Fig.11A 5393670 69 X-XXSGVXXX-XQXXRX-XDW-X-XXRWMHDXXX-XYXXSCTVXX--XR-XXQ-X- 116
SEQIDNO1 09/888,224 181 NLAAERIGRAILEVAQWIFVEGTQFTPEIDGRYKWHNAWWGGNLMGVRKYPVNLPR 240

Fig.11A 5393670 117 XH-XXX-X-X-X-XXEX-XXX--XX-XX--XXCFIX-XXXXXXXX-X---AXXVVDX 158
SEQIDNO1 09/888,224 241 DKVVYSPQVYGSEVYQPYFDPGEGFPDNLPEIWHHFFYKLDLGYPVVIGEFCKYGH 300

Fig.11A 5393670 159 RAXSXXIXXQ--Y--MPSXXSGXX--SVVXX-X-XXXXSX-XXXXXVMXX 211
SEQIDNO1 09/888,224 301 GGDPRDVWQKIIDWMIQNKCFDFWNNPNNGDTGIGKDWTTIWEDKNNKRM 360

Fig.11A 5393670 212 XG-XXAXASTXDLXS--X-XX---XXXXXXXXA--XAXXSQXWXXGA--X-X- 256
SEQIDNO1 09/888,224 361 DSCSNATAPSVPTTTTTTSTPTTTTTTSTPTTTQTPTTTPTTTTTPSNNV 420

Fig.11A 5393670 256 -XXXX-XTAGAN--X-AAXXXXXPVXXXX-XXXTX-XXXXXXSHGFXLQDQX 309
SEQIDNO1 09/888,224 421 FEIVNVLPTSSQVETSVEVVGTCAXRLGSSEPLSR*NRKRHHGPRLGGRLQ 480

Fig.11A 5393670 310 SW-XQLXXXX-NXXXXX-XX-XXXARPX-C-X-XXS-XXX-LPLPW-XX--GYXXX 358
SEQIDNO1 09/888,224 481 DCTPHWNRQHKDGDKERGAQGYKPEHQHSEV*HNGIPGGHIERALGPANKRSELR 540

Fig.11A 5393670 359 XXXX--PXIXX-X-XXQD---HHHX-XXXVXX-HGQXXSX-XXXCEHHPQVP 408
SEQIDNO1 09/888,224 541 PDKGLPSEIT*HKVARKEPGKQLRL*GLALQGCQHEITRGGLRDNGTALHRGR 600

Fig.11A 5393670 409 AXNXRXXPAAQPGXX-X-X-X-S-XV--XAPPPXXXLKAX--XLAT-XGXXX-XXX-- 456
SEQIDNO1 09/888,224 601 LSCGLQGA*SHR*CSNRRWKACKPDF*ALRHSGCRMVHLQAN*ELRLRGCVRLH 660

Fig.11A 5393670 456 --QXXW-XAXXHLRQQPXX-XXX-LDSXQX-XRXX-X-XQXX-EGX--IQX- 504
SEQIDNO1 09/888,224 661 QIHNS*QLPRLPHPLPDPGIRYRDIHQRVHLIPMHSGRKVDP*QVQVHPGRNNG 720

Fig.11A 5393670 505 SX-XX-X--XX-X---PXXXXVXX--XSIRWGDIGXYELDCAPAPCVQHDXFRX- 552
SEQIDNO1 09/888,224 721 H*GHSSRRRGPPASRFHNIADDFNHNPAHYHYD*DFNHHYNHLT*DNHRTCSGRN 780

Fig.11A 5393670 553 YTEXARLRAAARRXHGQX-XXXWXTXXVXXXXXXRXAXXVPV*XTTXXXQCE-* 610
SEQIDNO1 09/888,224 781 *AQVPGWAV*GPN*QGRRKPRVL*RNKPVEHTER*KLRRDDLQLE*RGSPLRPG* 840

Fig.11A 5393670 611 SVD 613
SEQIDNO1 09/888,224 841 YMM 843